

# SEQUENCE LISTING

<110> SOLOMON, Beka  
FRENKEL, Dan  
HANAN, Eilat

<120> AGENTS AND COMPOSITIONS AND METHODS UTILIZING SAME USEFUL IN  
DIAGNOSING AND/OR TREATING OR PREVENTING PLAQUE FORMING DISEASES

<130> SOLOMON=2C

<140> 09/830,954

<141> 2001-05-03

<150> PCT/IL00/00518

<151> 2000-08-31

<150> 09/629,971

<151> 2000-07-31

<150> US 09/473,653

<151> 1999-12-29

<150> US 60/152,417

<151> 1999-09-03

<160> 29

<170> PatentIn version 3.0

<210> 1

<211> 4

<212> PRT

<213> Artificial Sequence Sequence

<220>

<223> synthetic peptide

<400> 1

Glu Phe Arg His

1

<210> 2

<211> 15

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetic peptide

<400> 2

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser  
1 5 10 15

<210> 3

<211> 43

<212> PRT  
 <213> Artificial Sequence

<220>  
 <223> synthetic peptide

<400> 3

Asp Ala Glu Phe Arg His Asp Ser Gly Tyr Glu Val His His Gln Lys  
 1 5 10 15

Leu Val Phe Phe Ala Glu Asp Val Gly Ser Asn Lys Gly Ala Ile Ile  
 20 25 30

Gly Leu Met Val Gly Gly Val Val Ile Ala Thr  
 35 40

<210> 4  
 <211> 4  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> synthetic peptide

<400> 4

Trp Val Leu Asp  
 1

<210> 5  
 <211> 717  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> (1)..(717)

<400> 5

cag gtc aaa ctg cag gag tca ggg gct gag ctg gtg agg cct ggg gtc 48  
 Gln Val Lys Leu Gln Glu Ser Gly Ala Glu Leu Val Arg Pro Gly Val  
 1 5 10 15

tca gtg aag att tcc tgc aag ggt tct ggc tac aca ttc act gat tat 96  
 Ser Val Lys Ile Ser Cys Lys Gly Ser Gly Tyr Thr Phe Thr Asp Tyr  
 20 25 30

gct atg cac tgg gtg aag cag agt cat gca aag agt cta gag tgg att 144  
 Ala Met His Trp Val Lys Gln Ser His Ala Lys Ser Leu Glu Trp Ile  
 35 40 45

gga gtt att agt act tac tat ggt gat gct agc tac aac cag aag ttc 192  
 Gly Val Ile Ser Thr Tyr Tyr Gly Asp Ala Ser Tyr Asn Gln Lys Phe  
 50 55 60

aag ggc aag gcc aca atg act gta gac aaa tcc tcc agc aca gcc tat 240  
 Lys Gly Lys Ala Thr Met Thr Val Asp Lys Ser Ser Ser Thr Ala Tyr  
 65 70 75 80

atg gaa ctt gcc aga ctg aca tct gag gat tct gcc atc tat tac tgt 288  
 Met Glu Leu Ala Arg Leu Thr Ser Glu Asp Ser Ala Ile Tyr Tyr Cys  
 85 90 95

gca aga ggg gct act atg tcc tac ttt gac tac tgg ggc caa gtg acc 336  
 Ala Arg Gly Ala Thr Met Ser Tyr Phe Asp Tyr Trp Gly Gln Val Thr  
 100 105 110

acg gtc acc gtc tcc tca ggt gga ggc ggt tca ggc gga gtt ggc tct 384  
 Thr Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Val Gly Ser  
 115 120 125

ggc ggt ggc gga tgc gac atc gag ctc act cag tct cca gca atc atg 432  
 Gly Gly Gly Gly Ser Asp Ile Glu Leu Thr Gln Ser Pro Ala Ile Met  
 130 135 140

tct gca tct cca ggg gag aag gtc acc atg acc tgc agt gcc agc tca 480  
 Ser Ala Ser Pro Gly Glu Lys Val Thr Met Thr Cys Ser Ala Ser Ser  
 145 150 155 160

agt ata agt tac atg cac tgg tat cag cag aag cca ggc acc tcc ccc 528  
 Ser Ile Ser Tyr Met His Trp Tyr Gln Lys Pro Gly Thr Ser Pro  
 165 170 175

aaa aga tgg att tat gac aca tcc aaa ctg gct tct gga gtc cct gct 576  
 Lys Arg Trp Ile Tyr Asp Thr Ser Lys Leu Ala Ser Gly Val Pro Ala  
 180 185 190

cgc ttc agt ggc agt ggg tct ggg acc tct tat tct ctc aca atc agc 624  
 Arg Phe Ser Gly Ser Gly Ser Gly Thr Ser Tyr Ser Leu Thr Ile Ser  
 195 200 205

agc atg gag gct gaa gat gct gcc act tat tac tgc cat cag cgg agt 672  
 Ser Met Glu Ala Glu Asp Ala Ala Thr Tyr Tyr Cys His Gln Arg Ser  
 210 215 220

agt tac cca ttc acg ttc gga ggg ggg gcc aag ctg gaa ata aaa 717  
 Ser Tyr Pro Phe Thr Phe Gly Gly Gly Ala Lys Leu Glu Ile Lys  
 225 230 235

<210> 6  
 <211> 239  
 <212> PRT  
 <213> Homo sapiens

<400> 6

Gln Val Lys Leu Gln Glu Ser Gly Ala Glu Leu Val Arg Pro Gly Val  
 1 5 10 15

Ser Val Lys Ile Ser Cys Lys Gly Ser Gly Tyr Thr Phe Thr Asp Tyr  
 20 25 30

Ala Met His Trp Val Lys Gln Ser His Ala Lys Ser Leu Glu Trp Ile  
35 40 45

Gly Val Ile Ser Thr Tyr Tyr Gly Asp Ala Ser Tyr Asn Gln Lys Phe  
50 55 60

Lys Gly Lys Ala Thr Met Thr Val Asp Lys Ser Ser Ser Thr Ala Tyr  
65 70 75 80

Met Glu Leu Ala Arg Leu Thr Ser Glu Asp Ser Ala Ile Tyr Tyr Cys  
85 90 95

Ala Arg Gly Ala Thr Met Ser Tyr Phe Asp Tyr Trp Gly Gln Val Thr  
100 105 110

Thr Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Val Gly Ser  
115 120 125

Gly Gly Gly Gly Ser Asp Ile Glu Leu Thr Gln Ser Pro Ala Ile Met  
130 135 140

Ser Ala Ser Pro Gly Glu Lys Val Thr Met Thr Cys Ser Ala Ser Ser  
145 150 155 160

Ser Ile Ser Tyr Met His Trp Tyr Gln Gln Lys Pro Gly Thr Ser Pro  
165 170 175

Lys Arg Trp Ile Tyr Asp Thr Ser Lys Leu Ala Ser Gly Val Pro Ala  
180 185 190

Arg Phe Ser Gly Ser Gly Ser Gly Thr Ser Tyr Ser Leu Thr Ile Ser  
195 200 205

Ser Met Glu Ala Glu Asp Ala Ala Thr Tyr Tyr Cys His Gln Arg Ser  
210 215 220

Ser Tyr Pro Phe Thr Phe Gly Gly Gly Ala Lys Leu Glu Ile Lys  
225 230 235

<210> 7  
<211> 6  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> synthetic peptide

<400> 7

Tyr Tyr Glu Phe Arg His  
1 5

<210> 8  
<211> 15  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> synthetic peptide

<400> 8

Val His Glu Pro His Glu Phe Arg His Val Ala Leu Asn Pro Val  
1 5 10 15

<210> 9  
<211> 3  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> synthetic peptide

<400> 9

Lys Leu His  
1

<210> 10  
<211> 45  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> primer

<220>  
<221> misc\_feature  
<223> "n" at position 17 is unknown

<400> 10  
ccccctccg aacgtsnatg ggtaactcga tcgctgatgg cagta

45

<210> 11  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>

<223> primer

<400> 11

atctatgcgg cccagccggc catg

24

<210> 12

<211> 38

<212> DNA

<213> Artificial Sequence

<220>

<223> primer

<400> 12

gtggtgctga gtggatccta tactacactg ccaccggg

38

<210> 13

<211> 58

<212> DNA

<213> Artificial Sequence

<220>

<223> primer

<400> 13

agctccgatg ctgaattcgg tgatagcggc tacgaagtgc atcatcagaa acctgcag

58

<210> 14

<211> 52

<212> DNA

<213> Artificial Sequence

<220>

<223> primer

<400> 14

ggtttctgat gatgcacttc gtagccgcta tcatgacgaa attcagcatc gg

52

<210> 15

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetic peptide

<400> 15

His Gln Arg Ser Ser Tyr Pro Cys Thr

1

5

<210> 16

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetic peptide

<400> 16

His Gln Arg Ser Ser Tyr Pro Cys Thr  
1 5

<210> 17

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetic peptide

<400> 17

His Gln Arg Ser Ser Tyr Pro Phe Thr  
1 5

<210> 18

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetic peptide

<400> 18

His Gln Arg Ser Ser Tyr Pro Tyr Thr  
1 5

<210> 19

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetic peptide

<400> 19

His Gln Arg Ser Ser Tyr Pro Phe Thr  
1 5

<210> 20

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetic peptide

<400> 20

His Gln Arg Ser Ser Tyr Pro Ser Thr  
1 5

<210> 21  
<211> 15  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> synthetic peptide

<400> 21

Asp Thr Glu Phe Arg His Ser Ser Asn Asn Phe Ser Ala Val Arg  
1 5 10 15

<210> 22  
<211> 15  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> synthetic peptide

<400> 22

Ser Thr Glu Phe Arg His Gln Thr Thr Pro Leu His Pro Asn Ser  
1 5 10 15

<210> 23  
<211> 15  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> synthetic peptide

<400> 23

Lys Glu Pro Arg His His Ile Gln His His Glu Arg Val Ile Arg  
1 5 10 15

<210> 24  
<211> 15  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> synthetic peptide

<400> 24

Ser Ala Ala Asp Phe Arg His Gly Ser Pro Pro Ile Ser Ala Phe  
1 5 10 15

<210> 25  
<211> 21



<212> PRT  
<213> Artificial Sequence

<220>  
<223> synthetic peptide

<400> 25

Lys Thr Asn Met Lys His Met Ala Gly Ala Ala Ala Ala Gly Ala Val  
1 5 10 15

Val Gly Gly Leu Gly  
20

<210> 26  
<211> 4  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> synthetic peptide

<400> 26

Asp Met Lys His  
1

<210> 27  
<211> 357  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> synthetic construct

<220>  
<221> CDS  
<222> (1)..(357)

<400> 27

ggc ggt tca ggc gga gtt ggc tct ggc ggt ggc gga tcg gac atc gag 48  
Gly Gly Ser Gly Gly Val Gly Ser Gly Gly Gly Gly Ser Asp Ile Glu  
1 5 10 15

ctc act cag tct cca gca atc atg tct gca tct cca ggg gag aag gtc 96  
Leu Thr Gln Ser Pro Ala Ile Met Ser Ala Ser Pro Gly Glu Lys Val  
20 25 30

acc atg acc tgc agt gcc agc tca agt ata agt tac atg cac tgg tat 144  
Thr Met Thr Cys Ser Ala Ser Ser Ser Ile Ser Tyr Met His Trp Tyr  
35 40 45

cag cag aag cca ggc acc tcc ccc aaa aga tgg att tat gac aca tcc 192  
Gln Gln Lys Pro Gly Thr Ser Pro Lys Arg Trp Ile Tyr Asp Thr Ser  
50 55 60

aaa ctg gct tct gga gtc cct gct cgc ttc agt ggc agt ggg tct ggg 240  
 Lys Leu Ala Ser Gly Val Pro Ala Arg Phe Ser Gly Ser Gly Ser Gly  
 65 70 75 80

acc tct tat tct ctc aca atc agc agc atg gag gct gaa gat gct gcc 288  
 Thr Ser Tyr Ser Leu Thr Ile Ser Ser Met Glu Ala Glu Asp Ala Ala  
 85 90 95

act tat tac tgc cat cag cgg agt agt tac cca ttc acg ttc gga ggg 336  
 Thr Tyr Tyr Cys His Gln Arg Ser Ser Tyr Pro Phe Thr Phe Gly Gly  
 100 105 110

ggg gcc aag ctg gaa ata aaa 357  
 Gly Ala Lys Leu Glu Ile Lys  
 115

<210> 28  
 <211> 119  
 <212> PRT  
 <213> Artificial Sequence

<400> 28

<220>  
 <223> synthetic construct

Gly Gly Ser Gly Gly Val Gly Ser Gly Gly Gly Gly Ser Asp Ile Glu  
 1 5 10 15

Leu Thr Gln Ser Pro Ala Ile Met Ser Ala Ser Pro Gly Glu Lys Val  
 20 25 30

Thr Met Thr Cys Ser Ala Ser Ser Ser Ile Ser Tyr Met His Trp Tyr  
 35 40 45

Gln Gln Lys Pro Gly Thr Ser Pro Lys Arg Trp Ile Tyr Asp Thr Ser  
 50 55 60

Lys Leu Ala Ser Gly Val Pro Ala Arg Phe Ser Gly Ser Gly Ser Gly  
 65 70 75 80

Thr Ser Tyr Ser Leu Thr Ile Ser Ser Met Glu Ala Glu Asp Ala Ala  
 85 90 95

Thr Tyr Tyr Cys His Gln Arg Ser Ser Tyr Pro Phe Thr Phe Gly Gly  
 100 105 110

Gly Ala Lys Leu Glu Ile Lys  
 115

<210> 29  
<211> 21  
<212> PRT  
<213> Mus sp.

<400> 29

Lys Thr Asn Leu Lys His Val Ala Gly Ala Ala Ala Ala Gly Ala Val  
1 5 10 15

Val Gly Gly Leu Gly  
20